IN THE CLAIMS:

Please amend withdrawn claim 1 and pending claim 13 as shown below.

1. (Withdrawn - currently amended) A method of detecting *Mycobacterium* species present in a biological sample, comprising the steps of:

providing a biological sample containing nucleic acid from at least one *Mycobacterium* species comprising a *Mycobacterium* 16S ribosomal RNA (rRNA) or DNA encoding a *Mycobacterium* 16S rRNA;

amplifying the *Mycobacterium* 16S rRNA or *Mycobacterium* DNA encoding the Mycobacterium 16S rRNA in an *in vitro* nucleic acid amplification mixture comprising at least one polymerase activity, and a combination of at least ~~two primers selected from the group consisting of a first primer of SEQ ID NO:11 and a second primer that is~~ one first oligonucleotide and at least one second oligonucleotide, wherein the first oligonucleotide consists of a promoter sequence and a sequence that hybridizes to a *Mycobacterium* 16S rRNA or DNA sequence, and the second oligonucleotide is an oligonucleotide consisting of 19 to 25 bases ~~that contains~~ made up of contiguous bases 1 to 18 of SEQ ID NO:24 and optionally three to seven bases 5' to the contiguous bases 1 to 18 of SEQ ID NO:24 and/or optionally one base 3' to the contiguous bases 1 to 18 of SEQ ID NO:24 to produce amplified *Mycobacterium* nucleic acid; and

detecting the amplified *Mycobacterium* nucleic acid by detecting a label associated with the amplified *Mycobacterium* nucleic acid.

2. (Withdrawn - Original) The method of Claim 1, further comprising in the steps of:

adding to the biological sample at least one capture oligonucleotide that

specifically
hybridizes to the *Mycobacterium* 16S rRNA and an immobilized nucleic acid that hybridizes to
the capture oligonucleotide under hybridizing conditions to produce a hybridization complex;
and

separating the hybridization complex from other components of the biological sample before the amplifying step.

3. (Withdrawn - Original) The method of Claim 1, wherein the amplifying step amplifies 16S rRNA or DNA encoding 16S rRNA from *M. tuberculosis* or a *Mycobacterium* other than *tuberculosis* (MOTT) species.

4. (Withdrawn - Original) The method of Claim 1, wherein the amplifying step amplifies 16S rRNA or DNA encoding 16S rRNA from *M. abscessus, M. africanum, M. asiaticum, M. avium, M. bovis, M. celatum, M. chelonae, M. flavescens, M. fortuitum, M. gastri, M. gordonae, M. haemophilum, M. intracellulare, M. interjectum, M. intermedium, M. kansasii, M. malmoense, M. marinum, M. non-chromogenicum, M. paratuberculosis, M. phlei, M. scrofulaceum, M. shimodei, M. simiae, M. smegmatis, M. szulgai, M. terrae, M. triviale, M. tuberculosis, M. ulcerans* or *M. xenopi.*

5. (Withdrawn - Original) The method of Claim 1, wherein the detecting step uses at least one probe that hybridizes specifically to the amplified *Mycobacterium* nucleic acid.

6. (Withdrawn - Original) The method of Claim 5, wherein the detecting step uses at least one labeled probe that hybridizes specifically to the amplified *Mycobacterium* nucleic acid.

7. (Withdrawn - Original) The method of Claim 5, wherein the detecting step uses a plurality of probes that hybridize specifically to the amplified *Mycobacterium* nucleic acid.

8. (Withdrawn - Previously amended) The method of Claim 1, wherein the amplifying step uses a combination of at least a first primer and a second primer, wherein the first primer consists of SEQ ID NO:11, and the second primer is selected from the group consisting of SEQ ID NO:21, SEQ NO:22, SEQ ID NO:23 and SEQ ID NO:24.

9. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:21.

10. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:22.

11. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:23.

12. (Withdrawn - Previously amended) The method of Claim 8, wherein the second primer consists of SEQ ID NO:24.

13. (Currently amended) A composition for amplifying in an in vitro amplification reaction a *Mycobacterium* 16S rRNA sequence or a DNA encoding 16S rRNA, comprising a combination of at least ~~two oligonucleotides~~ one first oligonucleotide and at least one second oligonucleotide, wherein [[a]] the first oligonucleotide ~~contains~~ consists of a promoter sequence and a sequence that hybridizes to a *Mycobacterium* 16S rRNA or DNA sequence, and [[a]] wherein the second oligonucleotide is an

oligonucleotide consisting of 19 to 25 bases ~~that contains~~ made up of contiguous bases 1 to 18 of SEQ ID NO:24 and optionally three to seven bases 5' to the contiguous bases 1 to 18 of SEQ ID NO:24 and/or optionally one base 3' to the contiguous bases 1 to 18 of SEQ ID NO:24.

14. (Previously amended) The composition of Claim 13, wherein the composition comprises:

at least one first oligonucleotide consisting of SEQ ID NO:11, and

at least one second oligonucleotide consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 or SEQ ID NO:24.

15. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and

the at least one second oligonucleotide consisting of SEQ ID NO:21.

16. (Previously amended) A kit containing one or more oligonucleotides selected from the group consisting of SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24.

17. (Previously amended) The kit of claim 16, further containing an oligonucleotide consisting of SEQ ID NO:11.

18. (Previously amended) The kit of claim 17, containing

a first oligonucleotide consisting of SEQ ID NO:11, and

at least one second oligonucleotide consisting of SEQ ID NO:21, SEQ ID NO:22, or SEQ ID NO:23.

19. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and

the at least one second oligonucleotide consisting of SEQ ID NO:23.

20. (Previously amended) The composition of Claim 14, wherein the composition comprises:

the at least one first oligonucleotide consisting of SEQ ID NO:11, and

the at least one second oligonucleotide consisting of SEQ ID NO:24.